

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 19/5261221
Source: PCT
Date Processed by STIC: 2/27/06

ENTERED



PCT

RAW SEQUENCE LISTING DATE: 02/27/2006
PATENT APPLICATION: US/10/526,221 TIME: 14:37:32

Input Set : A:\265833US0XPCT.ST25.txt
Output Set: N:\CRF4\02272006\J526221.raw

(PS. 6)

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PATENT APPLICATION: US/10/526,221

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80	tcctggtgtc	cagttggaa	ctgttacagt	ttgcgttaagg	atcatgatac	tgctctcaaa	1560										
82	atgtttcaga	gagctatcca	actgaatgaa	agattcacat	atgcacatac	ccttggc	1620										
84	cacaggtttg	ccgcattgga	agaattcagag	gatgcagaga	gatgcattccg	gaaggctctg	1680										
86	ggcatagata	cgagacacta	taatgcattgg	tacggcttgc	aatgaccta	tcttcgtcag	1740										
88	gagaatttcg	agtttgcgc	gatcaattt	caactggctc	tccaaataaa	tccaaatct	1800										
90	tcaatcatca	tgtttacta	tggaaattgc	ttgcattgact	caaagagaaa	cgatgaggcg	1860										
92	ttgtatgtga	tggagaaggc	tgtactcact	gatgcaaaaga	atccgctccc	caagtaactac	1920										
94	aaggctcaca	tattaaccag	ccttaggtat	tatcacaaag	cacagaaagt	tttagaaagag	1980										
96	ctcaaagaat	gtgctcctca	agaaaggcagt	gtccatgcat	cgcttggcaa	aatatacaat	2040										
98	cagctaaagc	aatacgacaa	agccgtgtt	catttcggca	ttgctttgaa	tttaagccct	2100										
100	tctccatctg	atgctgtcaa	gataaaaggct	tacatggaga	ggttgataact	accagacgag	2160										
102	ctgggtacgg	aggaaaattt	gtagatttat	tgtgcaggta	atacaccaga	ttatgtttct	2220										
104	catataaccc	aaagtcatct	gtatattttc	tcatctttag	atcagtcttgc	tggactaacc	2280										
106	ctaaaacaaa	actgattata	taaacttaga	ggtaatatt	acagaaaatt	gtatagagtt	2340										
108	gggtttgaat	tttcatttct	tttccaagg	ggaacttttg	ttcaaaaaaaaa	aaaaaaaaaaa	2400										
110	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaa	aaaaaa	aaaaaa	2434										
113	<210>	SEQ ID NO:	2														
114	<211>	LENGTH:	728														
115	<212>	TYPE:	PRT														
116	<213>	ORGANISM:	Arabidopsis thaliana														
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121	1				5					10					15		
124	Phe	Met	Phe	Thr	Asn	Ala	Ile	Phe	Leu	Cys	Glu	Leu	Leu	Leu	Ala	Gln	
125						20				25					30		
128	Phe	Pro	Ser	Glu	Val	Asn	Leu	Gln	Leu	Leu	Ala	Arg	Cys	Tyr	Leu	Ser	
129						35				40			45				
132	Asn	Ser	Gln	Ala	Tyr	Ser	Ala	Tyr	Tyr	Ile	Leu	Lys	Gly	Ser	Lys	Thr	
133						50				55			60				
136	Pro	Gln	Ser	Arg	Tyr	Leu	Phe	Ala	Phe	Ser	Cys	Phe	Lys	Leu	Asp	Leu	
137						65				70			75			80	
140	Leu	Gly	Glu	Ala	Glu	Ala	Ala	Leu	Leu	Pro	Cys	Glu	Asp	Tyr	Ala	Glu	
141						85				90			95				
144	Glu	Val	Pro	Gly	Gly	Ala	Ala	Gly	His	Tyr	Leu	Leu	Gly	Leu	Ile	Tyr	
145						100				105			110				
148	Arg	Tyr	Ser	Gly	Arg	Lys	Asn	Cys	Ser	Ile	Gln	Gln	Phe	Arg	Met	Ala	
149						115				120			125				
152	Leu	Ser	Phe	Asp	Pro	Leu	Cys	Trp	Glu	Ala	Tyr	Gly	Glu	Leu	Cys	Ser	
153						130				135			140				
156	Leu	Gly	Ala	Ala	Glu	Glu	Ala	Ser	Thr	Val	Phe	Gly	Asn	Val	Ala	Ser	
157						145				150			155			160	
160	Gln	Arg	Leu	Gln	Lys	Thr	Cys	Val	Glu	Gln	Arg	Ile	Ser	Phe	Ser	Glu	
161						165				170			175				
164	Gly	Ala	Thr	Ile	Asp	Gln	Ile	Thr	Asp	Ser	Asp	Lys	Ala	Leu	Lys	Asp	
165						180				185			190				
168	Thr	Gly	Leu	Ser	Gln	Thr	Glu	His	Ile	Pro	Gly	Glu	Asn	Gln	Gln	Asp	
169						195				200			205				
172	Leu	Lys	Ile	Met	Gln	Gln	Pro	Gly	Asp	Ile	Pro	Pro	Asn	Thr	Asp	Arg	
173						210				215			220				

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176 Gln Leu Ser Thr Asn Gly Trp Asp Leu Asn Thr Pro Ser Pro Val Leu
177 225 230 235 240
180 Leu Gln Val Met Asp Ala Leu Pro Pro Leu Leu Leu Lys Asn Met Arg
181 245 250 255
184 Arg Pro Ala Val Glu Gly Ser Leu Met Ser Val His Gly Val Arg Val
185 260 265 270
188 Arg Arg Arg Asn Phe Phe Ser Glu Glu Leu Ser Ala Glu Ala Gln Glu
189 275 280 285
192 Glu Ser Gly Arg Arg Arg Ser Ala Arg Ile Ala Ala Arg Lys Lys Asn
193 290 295 300
196 Pro Met Ser Gln Ser Phe Gly Lys Asp Ser His Trp Leu His Leu Ser
197 305 310 315 320
200 Pro Ser Glu Ser Asn Tyr Ala Pro Ser Leu Ser Ser Met Ile Gly Lys
201 325 330 335
204 Cys Arg Ile Gln Ser Ser Lys Glu Val Ile Pro Asp Thr Val Thr Leu
205 340 345 350
208 Asn Asp Pro Ala Thr Thr Ser Gly Gln Ser Val Ser Asp Ile Gly Ser
209 355 360 365
212 Ser Val Asp Asp Glu Glu Lys Ser Asn Pro Ser Glu Ser Ser Pro Asp
213 370 375 380
216 Arg Phe Ser Leu Ile Ser Gly Ile Ser Glu Val Leu Ser Leu Leu Lys
217 385 390 395 400
220 Ile Leu Gly Asp Gly His Arg His Leu His Met Tyr Lys Cys Gln Glu
221 405 410 415
224 Ala Leu Leu Ala Tyr Gln Lys Leu Ser Gln Lys Gln Tyr Asn Thr His
225 420 425 430
228 Trp Val Leu Met Gln Val Gly Lys Ala Tyr Phe Glu Leu Gln Asp Tyr
229 435 440 445
232 Phe Asn Ala Asp Ser Ser Phe Thr Leu Ala His Gln Lys Tyr Pro Tyr
233 450 455 460
236 Ala Leu Glu Gly Met Asp Thr Tyr Ser Thr Val Leu Tyr His Leu Lys
237 465 470 475 480
240 Glu Glu Met Arg Leu Gly Tyr Leu Ala Gln Glu Leu Ile Ser Val Asp
241 485 490 495
244 Arg Leu Ser Pro Glu Ser Trp Cys Ala Val Gly Asn Cys Tyr Ser Leu
245 500 505 510
248 Arg Lys Asp His Asp Thr Ala Leu Lys Met Phe Gln Arg Ala Ile Gln
249 515 520 525
252 Leu Asn Glu Arg Phe Thr Tyr Ala His Thr Leu Cys Gly His Glu Phe
253 530 535 540
256 Ala Ala Leu Glu Glu Phe Glu Asp Ala Glu Arg Cys Tyr Arg Lys Ala
257 545 550 555 560
260 Leu Gly Ile Asp Thr Arg His Tyr Asn Ala Trp Tyr Gly Leu Gly Met
261 565 570 575
264 Thr Tyr Leu Arg Gln Glu Lys Phe Glu Phe Ala Gln His Gln Phe Gln
265 580 585 590
268 Leu Ala Leu Gln Ile Asn Pro Arg Ser Ser Val Ile Met Cys Tyr Tyr
269 595 600 605
272 Gly Ile Ala Leu His Glu Ser Lys Arg Asn Asp Glu Ala Leu Met Met

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273	610	615	620															
276	Met	Glu	Lys	Ala	Val	Leu	Thr	Asp	Ala	Lys	Asn	Pro	Leu	Pro	Lys	Tyr		
277	625		630		635		640											
280	Tyr	Lys	Ala	His	Ile	Leu	Thr	Ser	Leu	Gly	Asp	Tyr	His	Lys	Ala	Gln		
281					645				650					655				
284	Lys	Val	Leu	Glu	Glu	Leu	Lys	Glu	Cys	Ala	Pro	Gln	Glu	Ser	Ser	Val		
285						660			665			670						
288	His	Ala	Ser	Leu	Gly	Lys	Ile	Tyr	Asn	Gln	Leu	Lys	Gln	Tyr	Asp	Lys		
289						675			680			685						
292	Ala	Val	Leu	His	Phe	Gly	Ile	Ala	Leu	Asp	Leu	Ser	Pro	Ser	Pro	Ser		
293						690			695			700						
296	Asp	Ala	Val	Lys	Ile	Lys	Ala	Tyr	Met	Glu	Arg	Leu	Ile	Leu	Pro	Asp		
297						705			710			715			720			
300	Glu	Leu	Val	Thr	Glu	Glu	Asn	Leu										
301						725												
304	<210>	SEQ	ID	NO:	3													
305	<211>	LENGTH:	2401															
306	<212>	TYPE:	DNA															
307	<213>	ORGANISM:	Arabidopsis thaliana															
309	<400>	SEQUENCE:	3															
310	atgatggaga	atctactggc	gaattgtgtc	cagaaaaacc	ttaaccattt	tatgttcacc										60		
312	aatgctatct	tccttgcga	acttcttc	gcccaatttc	catctgaggt	qaacctgcaa										120		
314	ttgttagcca	gggttactt	gagtaacagt	caagctata	gtgcata	tatccttaaa										180		
316	ggtcaaaaaa	cgcctcagtc	tcggatttta	tttgcattct	catgctttaa	gttggatctt										240		
318	cttggagagg	ctgaagctgc	attgttgc	ttgtgaagatt	atgctgaaga	agttcctgg										300		
320	ggtcagctg	ggcattatct	tcttggtctt	atatatagat	attctggag	gaagaactgt										360		
322	tcaatacacac	agtttaggat	ggcattgtca	tttgcattt	tgtgttgg	agcatatgg										420		
324	gaactttgt	gtttaggtgc	cgctgaagaa	gcctcaacag	ttttcgggaa	tgttgcttcc										480		
326	cagcgtctta	aaacttgtgt	agaacaaaga	ataagcttct	cagaaggagc	aaccatagac										540		
328	cagattacag	attctgtataa	ggccttaaaa	gatacagg	tatcgaaac	agaaacacatt										600		
330	ccaggagaga	accaacaaga	tctgaaaatt	atgcagcgc	ctggagat	tccaccaat										660		
332	actgacagggc	aacttagtac	aaacggatgg	gacttgaaca	caccccttc	agtgc										720		
334	caggtaatgg	atgctccacc	gcctctgc	cttaagaata	tgcgtcg	tc	agcagtgg									780		
336	ggatcttga	tgtctgtaca	ttggagtgcgt	gtgcgtcgaa	gaaaactttt	tagtgaagaa										840		
338	ttgtcagcag	aggctcaaga	agaatctgg	cgcccccgt	gtgctagaat	agcagcaagg										900		
340	aaaaagaatc	ctatgtcgca	gtcattttg	aaagattccc	attggttaca	tcttcac										960		
342	tccgagtcaa	actatgcacc	ttcttcttcc	tcgatgattt	gaaaatgcag	aatccaaagc										1020		
344	agcaaagaag	caacgacgtc	aggccagtc	gtaagtgaca	ctggaaagctc	tgttgc										1080		
346	gaggaaaagt	caaattcttag	tgaatcttcc	ccggatcg	tcagc	ttcttgc										1140		
348	tcagaagtgc	taagcattct	gaaaattctt	ggagatggcc	acaggcattt	acatatgtac										1200		
350	aagtgtcagg	aagtttgc	ggcataatcaa	aagctatctc	agaaacaata	caatacacac										1260		
352	tgggttctca	tgcagggttgg	aaaagcatat	tttgc	aagactactt	caacgctgac										1320		
354	tcttcccttta	ctcttgctca	tcaaaaagtat	ccttgc	tgg	ggat										1380		
356	tccactgttc	tttgc	aaaagaagag	atgagg	gtc	atgg										1440		
358	atttcagtttgc	tgc	aaaatcc	ttgg	tttgc	tttgc										1500		
360	cgttaaggatc	atgatactgc	tctcaaaatg	tttgc	atgg	atgg										1560		
362	ttcacatatg	cacataccct	ttgtggcc	gat	tttgc	tttgc										1620		
364	gcagagagat	gctaccggaa	ggctctggc	atgatacga	gacactataa	tgc	atgg									1680		
366	ggtcttggaa	tgacctatct	tcgtcagg	aaatcg	tttgc	tttgc										1740		

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368	ctggctctcc	aaataaaatcc	aagatcttca	gtcatcatgt	gttactatgg	aattgctttg	1800											
370	catgagtcaa	agagaaaacga	tgaggcggtg	atgatgatgg	agaaggctgt	actcactgat	1860											
372	gcaaagaatc	cgctccccaa	gtactacaag	gctcacatat	taaccagcct	aggtgattat	1920											
374	cacaaagcac	agaaagttt	agaagagctc	aaagaatgtg	ctcctcaaga	aaggcgtgtc	1980											
376	catgcacatcg	ttggcaaaat	atacaatcag	ctaaagcaat	acgacaaagc	cgtgttacat	2040											
378	ttcggcattt	cttggattt	aagcccttct	ccatctgtat	ctgtcaagat	aaaggcttac	2100											
380	atggagaggt	tgatactacc	agacgagctg	gtgacggagg	aaaatttta	gatttattgt	2160											
382	gcaggtata	caccagatta	tgtttctcat	ataacccaaa	gtcatctgtat	attttctca	2220											
384	tcttagatc	agtctgtgg	actaacccta	aaacaaaact	gattatataa	acttagaggg	2280											
386	taatattaca	gaaaatttta	tagagttggg	tttgaatttt	catttcttt	ccaagttgga	2340											
388	acttttgttc	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	2400											
390	a						2401											
393	<210>	SEQ ID NO:	4															
394	<211>	LENGTH:	716															
395	<212>	TYPE:	PRT															
396	<213>	ORGANISM:	Arabidopsis thaliana															
398	<400>	SEQUENCE:	4															
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401	1				5					10					15			
404	Phe	Met	Phe	Thr	Asn	Ala	Ile	Phe	Leu	Cys	Glu	Leu	Leu	Leu	Ala	Gln		
405						20			25						30			
408	Phe	Pro	Ser	Glu	Val	Asn	Leu	Gln	Leu	Leu	Ala	Arg	Cys	Tyr	Leu	Ser		
409						35			40			45						
412	Asn	Ser	Gln	Ala	Tyr	Ser	Ala	Tyr	Tyr	Ile	Leu	Lys	Gly	Ser	Lys	Thr		
413						50			55			60						
416	Pro	Gln	Ser	Arg	Tyr	Leu	Phe	Ala	Phe	Ser	Cys	Phe	Lys	Leu	Asp	Leu		
417	65					70			75			80						
420	Leu	Gly	Glu	Ala	Glu	Ala	Ala	Leu	Leu	Pro	Cys	Glu	Asp	Tyr	Ala	Glu		
421						85			90			95						
424	Glu	Val	Pro	Gly	Gly	Ala	Ala	Gly	His	Tyr	Leu	Leu	Gly	Leu	Ile	Tyr		
425						100			105			110						
428	Arg	Tyr	Ser	Gly	Arg	Lys	Asn	Cys	Ser	Ile	Gln	Gln	Phe	Arg	Met	Ala		
429						115			120			125						
432	Leu	Ser	Phe	Asp	Pro	Leu	Cys	Trp	Glu	Ala	Tyr	Gly	Glu	Leu	Cys	Ser		
433						130			135			140						
436	Leu	Gly	Ala	Ala	Glu	Glu	Ala	Ser	Thr	Val	Phe	Gly	Asn	Val	Ala	Ser		
437	145					150				155			160					
440	Gln	Arg	Leu	Lys	Thr	Cys	Val	Glu	Gln	Arg	Ile	Ser	Phe	Ser	Glu	Gly		
441						165			170			175						
444	Ala	Thr	Ile	Asp	Gln	Ile	Thr	Asp	Ser	Asp	Lys	Ala	Leu	Lys	Asp	Thr		
445						180			185			190						
448	Gly	Leu	Ser	Gln	Thr	Glu	His	Ile	Pro	Gly	Glu	Asn	Gln	Gln	Asp	Leu		
449						195			200			205						
452	Lys	Ile	Met	Gln	Gln	Pro	Gly	Asp	Ile	Pro	Pro	Asn	Thr	Asp	Arg	Gln		
453						210			215			220						
456	Leu	Ser	Thr	Asn	Gly	Trp	Asp	Leu	Asn	Thr	Pro	Ser	Pro	Val	Leu	Leu		
457	225					230				235			240					
460	Gln	Val	Met	Asp	Ala	Pro	Pro	Leu	Leu	Leu	Lys	Asn	Met	Arg	Arg			
461						245			250			255						

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 730,731,732,733 ✓
Seq#:6; Xaa Pos. 244,245
Seq#:7; N Pos. 911,1327,1792
Seq#:8; Xaa Pos. 260,399,554
Seq#:13; N Pos. 26

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:616 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:720
L:730 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:240
L:878 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:900
L:892 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:1320
L:906 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:1740
L:1022 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:256
L:1054 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:384
L:1094 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:544
L:1286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0